

## SEQUENCE LISTING

<110> SmithKline Beecham Biologicals S.A.

<120> Novel compounds

<130> BM45394

<160> 6

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 969

<212> DNA

<213> *Moraxella catarrhalis*

<400> 1

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agtacctcg gttcgggcag tcatcgact tcaggttcag gtggttggc aataggttca	180
caggttatca cggacagtca gggcttacca aatcgctatc aggtgaagca gggcgatact	240
gtcagtaaga ttgctcagcg ttatggatta aattggcgtg agattggaca cattaataat	300
ctaaatagca gttatacgat ttatacaggt caatggctga ctttatggtc aggtgatctc	360
aaggtgcgtg agcgttagtat cagctctggt gtgaatacag ctcacacacc ttcgcctgtg	420
gcggttcagt caagcagacc accagtacag cagcatcctg ccgtacaaaa acccacgcca	480
cctgttgtg tggtaaaaaa acccacacccg actccgcctg tggttcagca gccagcacca	540
gttgccccac cagtgacaga agcaccattt gccacgggta gctcagggtt gatgcaattt	600
cgctatcctg ttggtgcgac caatccagtg gttcgacgct ttggtaacggc gacagtggcc	660
ggctcaactg ttaccagtaa tggcatgtgg ttttctggac gagatggcga ttttaattaac	720
gccagtaatg cagggcacagt cattcaagct gatcacaata tggacgggc gagtattgtg	780
attcagcata ccaatggatt tgtttcaagc tatatccata ttaaggacgc tcaagttaaa	840
acaggcgtata cgggtgcgtac cggtcagcgt attgcaagca tgaaaaatca gccaagcgggt	900
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<210> 2

<211> 322

&lt;212&gt; PRT

<213> *Moraxella catarrhalis*

&lt;400&gt; 2

Met Thr Val Thr Ile Ala Ile Asn Ser Gln Asn Gln Lys Pro Ile Lys  
1 5 10 15  
Arg Leu Gly Leu Ile Phe Gly Val Ile Thr Thr Cys Ile Leu Ala Gly  
20 25 30  
Cys Ala Ser Lys Pro Thr Tyr Asn Ser Thr Ser Gly Ser Gly Ser His  
35 40 45  
Arg Thr Ser Gly Ser Gly Gly Leu Ala Ile Gly Ser Gln Val Ile Thr  
50 55 60  
Asp Ser Gln Gly Val Pro Asn Arg Tyr Gln Val Lys Gln Gly Asp Thr  
65 70 75 80  
Val Ser Lys Ile Ala Gln Arg Tyr Gly Leu Asn Trp Arg Glu Ile Gly  
85 90 95  
His Ile Asn Asn Leu Asn Ser Ser Tyr Thr Ile Tyr Thr Gly Gln Trp  
100 105 110  
Leu Thr Leu Trp Ser Gly Asp Leu Lys Val Arg Glu Arg Ser Ile Ser  
115 120 125  
Ser Gly Val Asn Thr Ala His Thr Pro Ser Pro Val Ala Val Gln Ser  
130 135 140  
Ser Arg Pro Pro Val Gln Gln His Pro Ala Val Gln Lys Pro Thr Pro  
145 150 155 160  
Pro Val Val Val Val Lys Lys Pro Thr Pro Thr Pro Val Val Gln  
165 170 175  
Gln Pro Ala Pro Val Ala Pro Pro Val Thr Glu Ala Pro Phe Ala Thr  
180 185 190  
Gly Ser Ser Gly Val Met Gln Phe Arg Tyr Pro Val Gly Ala Thr Asn  
195 200 205  
Pro Val Val Arg Arg Phe Gly Thr Ala Thr Val Ala Gly Ser Thr Val  
210 215 220  
Thr Ser Asn Gly Met Trp Phe Ser Gly Arg Asp Gly Asp Leu Ile Asn  
225 230 235 240  
Ala Ser Asn Ala Gly Thr Val Ile Gln Ala Asp His Asn Met Asp Gly  
245 250 255  
Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile  
260 265 270  
His Ile Lys Asp Ala Gln Val Lys Thr Gly Asp Thr Val Arg Thr Gly  
275 280 285

Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Ala Ala Leu Phe  
 290 295 300  
 Glu Phe Arg Ile Ser Arg Asn Gly Val Tyr Val Asp Pro Leu Thr Val  
 305 310 315 320  
 Leu Lys

<210> 3  
 <211> 966  
 <212> DNA  
 <213> *Moraxella catarrhalis*

<400> 3

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agtacctcag	gttcgggcag	tcatcgtact	tcaggttcag	gtggtttgc	aatagggtca	180
caggttatca	cggacagtca	gggcgtacca	aatcgctatc	aggtgaagca	gggcgatact	240
gtcagtaaga	ttgctcagcg	ttatggatta	aattggcgtg	agattggaca	cattaataat	300
ctaaatagcg	gttatacgtat	ttatacaggt	caatggctga	ctttatggtc	aggtgatctc	360
aaggtgtcg	agcgttagtat	cagctctgg	gtgaatacag	ctcacacacc	ttcgccctgtg	420
gcggttcagt	caagcagacc	accagtacag	cagcatcctg	ccgtacaaaa	acccacgcca	480
cctgttgg	tggtaaaaaa	acccacaccg	actccgcctg	tggttcagca	gccagcacca	540
gttgccccac	cagtgcacaga	agcaccattt	gccacgggta	gctcagggt	gatgcaattt	600
cgctatcctg	ttgggtgcac	caatccagtg	tttcgacgct	ttggtaacggc	gacagtggcc	660
ggctcaactg	ttaccagtaa	tggcatgtgg	ttttctggac	gagatggcga	ttaattaac	720
gccagtaatg	caggcacagt	cattcaagct	gatcacaata	tggacgggac	gagtattgtg	780
attcagcata	ccaatggatt	tgttcaagc	tatatccata	ttaaggacgc	tcaagttaaa	840
acaggcgata	cgggtgcgtac	cggtcagcgt	attgcaagca	tgaaaaatca	gccaagcggt	900
gcggcactat	ttgaatttag	aatttctaga	aatggcgtgt	atgttgatcc	attgacagta	960
cttaaa						966

<210> 4  
 <211> 322  
 <212> PRT  
 <213> *Moraxella catarrhalis*

<400> 4

Met	Thr	Val	Thr	Ile	Ala	Ile	Asn	Ser	Gln	Asn	Gln	Lys	Pro	Ile	Lys
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20	25	30
Cys Ala Ser Lys Pro Thr Tyr Asn Ser Thr Ser Gly Ser Gly Ser His		
35	40	45
Arg Thr Ser Gly Ser Gly Gly Leu Ala Ile Gly Ser Gln Val Ile Thr		
50	55	60
Asp Ser Gln Gly Val Pro Asn Arg Tyr Gln Val Lys Gln Gly Asp Thr		
65	70	75
Val Ser Lys Ile Ala Gln Arg Tyr Gly Leu Asn Trp Arg Glu Ile Gly		
85	90	95
His Ile Asn Asn Leu Asn Ser Gly Tyr Thr Ile Tyr Thr Gly Gln Trp		
100	105	110
Leu Thr Leu Trp Ser Gly Asp Leu Lys Val Arg Glu Arg Ser Ile Ser		
115	120	125
Ser Gly Val Asn Thr Ala His Thr Pro Ser Pro Val Ala Val Gln Ser		
130	135	140
Ser Arg Pro Pro Val Gln Gln His Pro Ala Val Gln Lys Pro Thr Pro		
145	150	155
Pro Val Val Val Val Lys Lys Pro Thr Pro Thr Pro Pro Val Val Gln		
165	170	175
Gln Pro Ala Pro Val Ala Pro Pro Val Thr Glu Ala Pro Phe Ala Thr		
180	185	190
Gly Ser Ser Gly Val Met Gln Phe Arg Tyr Pro Val Gly Ala Thr Asn		
195	200	205
Pro Val Val Arg Arg Phe Gly Thr Ala Thr Val Ala Gly Ser Thr Val		
210	215	220
Thr Ser Asn Gly Met Trp Phe Ser Gly Arg Asp Gly Asp Leu Ile Asn		
225	230	235
Ala Ser Asn Ala Gly Thr Val Ile Gln Ala Asp His Asn Met Asp Gly		
245	250	255
Ala Ser Ile Val Ile Gln His Thr Asn Gly Phe Val Ser Ser Tyr Ile		
260	265	270
His Ile Lys Asp Ala Gln Val Lys Thr Gly Asp Thr Val Arg Thr Gly		
275	280	285
Gln Arg Ile Ala Ser Met Lys Asn Gln Pro Ser Gly Ala Ala Leu Phe		
290	295	300
Glu Phe Arg Ile Ser Arg Asn Gly Val Tyr Val Asp Pro Leu Thr Val		
305	310	315
Leu Lys		320

<210> 5  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 5  
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<210> 6  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 6  
aggcagaggc tcgagttaa gtactgtcaa tggatcaaca ta 42